



PCT

## RAW SEQUENCE LISTING

DATE: 12/22/2004

PATENT APPLICATION: US/10/517,905

TIME: 16:05:53

Input Set : A:\335026.txt

Output Set: N:\CRF4\12222004\J517905.raw

3 <110> APPLICANT: Oregon Health & Science University  
 4 Michael, Heinrich Charles  
 5 Corless, Christopher Lee  
 6 Fletcher, Jonathan Alfred  
 7 Demetri, George D.  
 9 <120> TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR  
 RECEPTOR

10 ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS  
 12 <130> FILE REFERENCE: 899-65892-02  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/517,905  
 C--> 14 <141> CURRENT FILING DATE: 2004-12-10

14 <150> PRIOR APPLICATION NUMBER: US 60/389,107  
 15 <151> PRIOR FILING DATE: 2002-06-13  
 17 <150> PRIOR APPLICATION NUMBER: US 60/438,899  
 18 <151> PRIOR FILING DATE: 2003-01-08  
 20 <160> NUMBER OF SEQ ID NOS: 27  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 6633  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:

31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (395)..(3664)  
 34 <400> SEQUENCE: 1

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 37 gtaagagcaa aaagcgaagg cgcaatctgg aactgaggag attcggagcg cagggagttt 120  
 39 gagagaaact tttattttga agagaccaag gttgaggggg ggcttatttc ctgacagcta 180  
 41 tttacttaga gcaaatgatt agtttttagaa ggatggacta taacattgaa tcaattacaa 240  
 43 aacgcggttt ttgagcccat tactgttggg gctacagggg gagaaacagg aggagactgc 300  
 45 aagagatcat ttgggaaggc cgtgggcaag ctctttactc catgtgtggg acattcattg 360  
 47 cggaataaca tcggaggaga agtttccag agct atg ggg act tcc cat ccg gcg 415  
 48 Met Gly Thr Ser His Pro Ala  
 49 1 5  
 51 ttc ctg gtc tta ggc tgt ctt ctc aca ggg ctg agc cta atc ctc tgc 463  
 52 Phe Leu Val Leu Gly Cys Leu Leu Thr Gly Leu Ser Leu Ile Leu Cys  
 53 10 15 20  
 55 cag ctt tca tta ccc tct atc ctt cca aat gaa aat gaa aag gtt gtg 511  
 56 Gln Leu Ser Leu Pro Ser Ile Leu Pro Asn Glu Asn Glu Lys Val Val  
 57 25 30 35  
 59 cag ctg aat tca tcc ttt tct ctg aga tgc ttt ggg gag agt gaa gtg 559  
 60 Gln Leu Asn Ser Ser Phe Ser Leu Arg Cys Phe Gly Glu Ser Glu Val  
 61 40 45 50 55  
 63 agc tgg cag tac ccc atg tct gaa gaa gag agc tcc gat gtg gaa atc 607

**Does Not Comply  
 Corrected Diskette Needed**

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67 aga aat gaa gaa aac aac agc ggc ctt ttt gtg acg gtc ttg gaa gtg      655
68 Arg Asn Glu Glu Asn Asn Ser Gly Leu Phe Val Thr Val Leu Glu Val
69                               75                               80                               85
71 agc agt gcc tcg gcg gcc cac aca ggg ttg tac act tgc tat tac aac      703
72 Ser Ser Ala Ser Ala Ala His Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn
73                               90                               95                               100
75 cac act cag aca gaa gag aat gag ctt gaa ggc agg cac att tac atc      751
76 His Thr Gln Thr Glu Glu Asn Glu Leu Glu Gly Arg His Ile Tyr Ile
77                               105                               110                               115
79 tat gtg cca gac cca gat gta gcc ttt gta cct cta gga atg acg gat      799
80 Tyr Val Pro Asp Pro Asp Val Ala Phe Val Pro Leu Gly Met Thr Asp
81 120                               125                               130                               135
83 tat tta gtc atc gtg gag gat gat gat tct gcc att ata cct tgt cgc      847
84 Tyr Leu Val Ile Val Glu Asp Asp Asp Ser Ala Ile Ile Pro Cys Arg
85                               140                               145                               150
87 aca act gat ccc gag act cct gta acc tta cac aac agt gag ggg gtg      895
88 Thr Thr Asp Pro Glu Thr Pro Val Thr Leu His Asn Ser Glu Gly Val
89                               155                               160                               165
91 gta cct gcc tcc tac gac agc aga cag ggc ttt aat ggg acc ttc act      943
92 Val Pro Ala Ser Tyr Asp Ser Arg Gln Gly Phe Asn Gly Thr Phe Thr
93                               170                               175                               180
95 gta ggg ccc tat atc tgt gag gcc acc gtc aaa gga aag aag ttc cag      991
96 Val Gly Pro Tyr Ile Cys Glu Ala Thr Val Lys Gly Lys Lys Phe Gln
97                               185                               190                               195
99 acc atc cca ttt aat gtt tat gct tta aaa gca aca tca gag ctg gat      1039
100 Thr Ile Pro Phe Asn Val Tyr Ala Leu Lys Ala Thr Ser Glu Leu Asp
101 200                               205                               210                               215
103 cta gaa atg gaa gct ctt aaa acc gtg tat aag tca ggg gaa acg att      1087
104 Leu Glu Met Glu Ala Leu Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile
105                               220                               225                               230
107 gtg gtc acc tgt gct gtt ttt aac aat gag gtg gtt gac ctt caa tgg      1135
108 Val Val Thr Cys Ala Val Phe Asn Asn Glu Val Val Asp Leu Gln Trp
109                               235                               240                               245
111 act tac cct gga gaa gtg aaa ggc aaa ggc atc aca atg ctg gaa gaa      1183
112 Thr Tyr Pro Gly Glu Val Lys Gly Lys Gly Ile Thr Met Leu Glu Glu
113                               250                               255                               260
115 atc aaa gtc cca tcc atc aaa ttg gtg tac act ttg acg gtc ccc gag      1231
116 Ile Lys Val Pro Ser Ile Lys Leu Val Tyr Thr Leu Thr Val Pro Glu
117                               265                               270                               275
119 gcc acg gtg aaa gac agt gga gat tac gaa tgt gct gcc cgc cag gct      1279
120 Ala Thr Val Lys Asp Ser Gly Asp Tyr Glu Cys Ala Ala Arg Gln Ala
121 280                               285                               290                               295
123 acc agg gag gtc aaa gaa atg aag aaa gtc act att tct gtc cat gag      1327
124 Thr Arg Glu Val Lys Glu Met Lys Lys Val Thr Ile Ser Val His Glu
125                               300                               305                               310
127 aaa ggt ttc att gaa atc aaa ccc acc ttc agc cag ttg gaa gct gtc      1375
128 Lys Gly Phe Ile Glu Ile Lys Pro Thr Phe Ser Gln Leu Glu Ala Val

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131 aac ctg cat gaa gtc aaa cat ttt gtt gta gag gtg cgg gcc tac cca				1423
132 Asn Leu His Glu Val Lys His Phe Val Val Glu Val Arg Ala Tyr Pro				
133 330 335 340				
135 cct ccc agg ata tcc tgg ctg aaa aac aat ctg act ctg att gaa aat				1471
136 Pro Pro Arg Ile Ser Trp Leu Lys Asn Asn Leu Thr Leu Ile Glu Asn				
137 345 350 355				
139 ctc act gag atc acc act gat gtg gaa aag att cag gaa ata agg tat				1519
140 Leu Thr Glu Ile Thr Thr Asp Val Glu Lys Ile Gln Glu Ile Arg Tyr				
141 360 365 370 375				
143 cga agc aaa tta aag ctg atc cgt gct aag gaa gaa gac agt ggc cat				1567
144 Arg Ser Lys Leu Lys Leu Ile Arg Ala Lys Glu Glu Asp Ser Gly His				
145 380 385 390				
147 tat act att gta gct caa aat gaa gat gct gtg aag agc tat act ttt				1615
148 Tyr Thr Ile Val Ala Gln Asn Glu Asp Ala Val Lys Ser Tyr Thr Phe				
149 395 400 405				
151 gaa ctg tta act caa gtt cct tca tcc att ctg gac ttg gtc gat gat				1663
152 Glu Leu Leu Thr Gln Val Pro Ser Ser Ile Leu Asp Leu Val Asp Asp				
153 410 415 420				
155 cac cat ggc tca act ggg gga cag acg gtg agg tgc aca gct gaa ggc				1711
156 His His Gly Ser Thr Gly Gly Gln Thr Val Arg Cys Thr Ala Glu Gly				
157 425 430 435				
159 acg ccg ctt cct gat att gag tgg atg ata tgc aaa gat att aag aaa				1759
160 Thr Pro Leu Pro Asp Ile Glu Trp Met Ile Cys Lys Asp Ile Lys Lys				
161 440 445 450 455				
163 tgt aat aat gaa act tcc tgg act att ttg gcc aac aat gtc tca aac				1807
164 Cys Asn Asn Glu Thr Ser Trp Thr Ile Leu Ala Asn Asn Val Ser Asn				
165 460 465 470				
167 atc atc acg gag atc cac tcc cga gac agg agt acc gtg gag ggc cgt				1855
168 Ile Ile Thr Glu Ile His Ser Arg Asp Arg Ser Thr Val Glu Gly Arg				
169 475 480 485				
171 gtg act ttc gcc aaa gtg gag gag acc atc gcc gtg cga tgc ctg gct				1903
172 Val Thr Phe Ala Lys Val Glu Glu Thr Ile Ala Val Arg Cys Leu Ala				
173 490 495 500				
175 aag aat ctc ctt gga gct gag aac cga gag ctg aag ctg gtg gct ccc				1951
176 Lys Asn Leu Leu Gly Ala Glu Asn Arg Glu Leu Lys Leu Val Ala Pro				
177 505 510 515				
179 acc ctg cgt tct gaa ctc acg gtg gct gct gca gtc ctg gtg ctg ttg				1999
180 Thr Leu Arg Ser Glu Leu Thr Val Ala Ala Ala Val Leu Val Leu Leu				
181 520 525 530 535				
183 gtg att gtg atc atc tca ctt att gtc ctg gtt gtc att tgg aaa cag				2047
184 Val Ile Val Ile Ile Ser Leu Ile Val Leu Val Val Ile Trp Lys Gln				
185 540 545 550				
187 aaa ccg agg tat gaa att cgc tgg agg gtc att gaa tca atc agc ccg				2095
188 Lys Pro Arg Tyr Glu Ile Arg Trp Arg Val Ile Glu Ser Ile Ser Pro				
189 555 560 565				
191 gat gga cat gaa tat att tat gtg gac ccg atg cag ctg cct tat gac				2143
192 Asp Gly His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp				
193 570 575 580				

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196	Ser	Arg	Trp	Glu	Phe	Pro	Arg	Asp	Gly	Leu	Val	Leu	Gly	Arg	Val	Leu	
197		585					590					595					
199	ggg	tct	gga	gcg	ttt	ggg	aag	gtg	gtt	gaa	gga	aca	gcc	tat	gga	tta	2239
200	Gly	Ser	Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Gly	Thr	Ala	Tyr	Gly	Leu	
201	600					605				610					615		
203	agc	cgg	tcc	caa	cct	gtc	atg	aaa	gtt	gca	gtg	aag	atg	cta	aaa	ccc	2287
204	Ser	Arg	Ser	Gln	Pro	Val	Met	Lys	Val	Ala	Val	Lys	Met	Leu	Lys	Pro	
205					620					625				630			
207	acg	gcc	aga	tcc	agt	gaa	aaa	caa	gct	ctc	atg	tct	gaa	ctg	aag	ata	2335
208	Thr	Ala	Arg	Ser	Ser	Glu	Lys	Gln	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	
209				635					640				645				
211	atg	act	cac	ctg	ggg	cca	cat	ttg	aac	att	gta	aac	ttg	ctg	gga	gcc	2383
212	Met	Thr	His	Leu	Gly	Pro	His	Leu	Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	
213			650					655				660					
215	tgc	acc	aag	tca	ggc	ccc	att	tac	atc	atc	aca	gag	tat	tgc	ttc	tat	2431
216	Cys	Thr	Lys	Ser	Gly	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Cys	Phe	Tyr	
217		665				670					675						
219	gga	gat	ttg	gtc	aac	tat	ttg	cat	aag	aat	agg	gat	agc	ttc	ctg	agc	2479
220	Gly	Asp	Leu	Val	Asn	Tyr	Leu	His	Lys	Asn	Arg	Asp	Ser	Phe	Leu	Ser	
221	680				685					690				695			
223	cac	cac	cca	gag	aag	cca	aag	aaa	gag	ctg	gat	atc	ttt	gga	ttg	aac	2527
224	His	His	Pro	Glu	Lys	Pro	Lys	Lys	Glu	Leu	Asp	Ile	Phe	Gly	Leu	Asn	
225				700					705			710					
227	cct	gct	gat	gaa	agc	aca	cgg	agc	tat	gtt	att	tta	tct	ttt	gaa	aac	2575
228	Pro	Ala	Asp	Glu	Ser	Thr	Arg	Ser	Tyr	Val	Ile	Leu	Ser	Phe	Glu	Asn	
229				715				720				725					
231	aat	ggt	gac	tac	atg	gac	atg	aag	cag	gct	gat	act	aca	cag	tat	gtc	2623
232	Asn	Gly	Asp	Tyr	Met	Asp	Met	Lys	Gln	Ala	Asp	Thr	Thr	Gln	Tyr	Val	
233			730				735					740					
235	ccc	atg	cta	gaa	agg	aaa	gag	gtt	tct	aaa	tat	tcc	gac	atc	cag	aga	2671
236	Pro	Met	Leu	Glu	Arg	Lys	Glu	Val	Ser	Lys	Tyr	Ser	Asp	Ile	Gln	Arg	
237		745				750					755						
239	tca	ctc	tat	gat	cgt	cca	gcc	tca	tat	aag	aag	aaa	tct	atg	tta	gac	2719
240	Ser	Leu	Tyr	Asp	Arg	Pro	Ala	Ser	Tyr	Lys	Lys	Lys	Ser	Met	Leu	Asp	
241	760				765					770				775			
243	tca	gaa	gtc	aaa	aac	ctc	ctt	tca	gat	gat	aac	tca	gaa	ggc	ctt	act	2767
244	Ser	Glu	Val	Lys	Asn	Leu	Leu	Ser	Asp	Asp	Asn	Ser	Glu	Gly	Leu	Thr	
245				780					785			790					
247	tta	ttg	gat	ttg	ttg	agc	ttc	acc	tat	caa	gtt	gcc	cga	gga	atg	gag	2815
248	Leu	Leu	Asp	Leu	Leu	Ser	Phe	Thr	Tyr	Gln	Val	Ala	Arg	Gly	Met	Glu	
249				795				800				805					
251	ttt	ttg	gct	tca	aaa	aat	tgt	gtc	cac	cgt	gat	ctg	gct	gct	cgc	aac	2863
252	Phe	Leu	Ala	Ser	Lys	Asn	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	
253			810				815					820					
255	gtc	ctc	ctg	gca	caa	gga	aaa	att	gtg	aag	atc	tgt	gac	ttt	ggc	ctg	2911
256	Val	Leu	Leu	Ala	Gln	Gly	Lys	Ile	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	
257		825				830					835						
259	gcc	aga	gac	atc	atg	cat	gat	tcg	aac	tat	gtg	tcg	aaa	ggc	agt	acc	2959

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260	Ala Arg Asp Ile Met His Asp Ser Asn Tyr Val Ser Lys Gly Ser Thr	
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264	Phe Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Asn Leu	
265	860 865 870	
267	tac acc aca ctg agt gat gtc tgg tct tat ggc att ctg ctc tgg gag	3055
268	Tyr Thr Thr Leu Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu	
269	875 880 885	
271	atc ttt tcc ctt ggt ggc acc cct tac ccc ggc atg atg gtg gat tct	3103
272	Ile Phe Ser Leu Gly Gly Thr Pro Tyr Pro Gly Met Met Val Asp Ser	
273	890 895 900	
275	act ttc tac aat aag atc aag agt ggg tac cgg atg gcc aag cct gac	3151
276	Thr Phe Tyr Asn Lys Ile Lys Ser Gly Tyr Arg Met Ala Lys Pro Asp	
277	905 910 915	
279	cac gct acc agt gaa gtc tac gag atc atg gtg aaa tgc tgg aac agt	3199
280	His Ala Thr Ser Glu Val Tyr Glu Ile Met Val Lys Cys Trp Asn Ser	
281	920 925 930 935	
283	gag ccg gag aag aga ccc tcc ttt tac cac ctg agt gag att gtg gag	3247
284	Glu Pro Glu Lys Arg Pro Ser Phe Tyr His Leu Ser Glu Ile Val Glu	
285	940 945 950	
287	aat ctg ctg cct gga caa tat aaa aag agt tat gaa aaa att cac ctg	3295
288	Asn Leu Leu Pro Gly Gln Tyr Lys Lys Ser Tyr Glu Lys Ile His Leu	
289	955 960 965	
291	gac ttc ctg aag agt gac cat cct gct gtg gca cgc atg cgt gtg gac	3343
292	Asp Phe Leu Lys Ser Asp His Pro Ala Val Ala Arg Met Arg Val Asp	
293	970 975 980	
295	tca gac aat gca tac att ggt gtc acc tac aaa aac gag gaa gac aag	3391
296	Ser Asp Asn Ala Tyr Ile Gly Val Thr Tyr Lys Asn Glu Glu Asp Lys	
297	985 990 995	
299	ctg aag gac tgg gag ggt ggt ctg gat gag cag aga ctg agc gct	3436
300	Leu Lys Asp Trp Glu Gly Gly Leu Asp Glu Gln Arg Leu Ser Ala	
301	1000 1005 1010	
303	gac agt ggc tac atc att cct ctg cct gac att gac cct gtc cct	3481
304	Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp Ile Asp Pro Val Pro	
305	1015 1020 1025	
307	gag gag gag gac ctg ggc aag agg aac aga cac agc tgc cag acc	3526
308	Glu Glu Glu Asp Leu Gly Lys Arg Asn Arg His Ser Ser Gln Thr	
309	1030 1035 1040	
311	tct gaa gag agt gcc att gag acg ggt tcc agc agt tcc acc ttc	3571
312	Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser Ser Thr Phe	
313	1045 1050 1055	
315	atc aag aga gag gac gag acc att gaa gac atc gac atg atg gac	3616
316	Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met Met Asp	
317	1060 1065 1070	
319	gac atc ggc ata gac tct tca gac ctg gtg gaa gac agc ttc ctg	3661
320	Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe Leu	
321	1075 1080 1085	
323	taa ctggcggatt cgaggggttc cttccacttc tggggccacc tctggatccc	3714
325	gttcagaaaa ccaatttatt gcaatgcgga gggtgagagg aggacttggt tgatgtttaa	3774

(from sequence 19)

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6

tgtatttggt cttttttata g ca aca tca gag ctg gat cta gaa atg gaa 6183  
Ala Thr Ser Glu Leu Asp Leu Glu Met Glu  
insert → 210 215  
gct ctt aaa acc gtg tat aag tca ggg gaa acg att gtg gtc acc tgt 6231  
Ala Leu Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys  
220 225 230 235

The above is a sample of several  
amino acid numbers inserted in  
sequence 19.

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:19; N Pos. 36802,36803,36804,36805,36806,36807,36808,36809,36810,36811  
Seq#:19; N Pos. 36812,36813,36814,36815,36816,36817,36818,36819,36820,36821  
Seq#:19; N Pos. 36822,36823,36824,36825,36826,36827,36828,36829,36830,36831  
Seq#:19; N Pos. 36832,36833,36834,36835,36836,36837,36838,36839,36840,36841  
Seq#:19; N Pos. 36842,36843,36844,36845,36846,36847,36848,36849,36850,36851  
Seq#:19; N Pos. 36852,36853,36854,36855,36856,36857,36858,36859,36860,36861  
Seq#:19; N Pos. 36862,36863,36864,36865,36866,36867,36868,36869,36870,36871  
Seq#:19; N Pos. 36872,36873  
Seq#:19; N Pos. 59740,59742,59743,59744,59749,59750,59751,59752,59753,59754  
Seq#:19; N Pos. 59755,59759,59760,59765,59766,59776,59777,59778,59779,59780

**RAW SEQUENCE LISTING ERROR SUMMARY**  
**PATENT APPLICATION: US/10/517,905**

**DATE: 12/22/2004**  
**TIME: 16:05:54**

**Input Set : A:\335026.txt**  
**Output Set: N:\CRF4\12222004\J517905.raw**

Seq#:19; N Pos. 59781,59782,59783,59784,59785,59786,59787,59788,59789,59790  
Seq#:19; N Pos. 59791,59792,59793,59794,59795,59796,59797,59798,59799,59800  
Seq#:19; N Pos. 59801,59802,59803,59804,59805,59806,59807,59808,59809,59810  
Seq#:19; N Pos. 59811,59812,59813,59814,59815,59816,59817,59818,59819,59820  
Seq#:19; N Pos. 59821,59822,59823,59824,59825,59826,59827,59828,59829,59830  
Seq#:19; N Pos. 59831,59832,59833,59834,59835,59836,59837,59838,59839,59840  
Seq#:19; N Pos. 59841,59842,59843,59844,59845,59846,59847,59848,59849,59850

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/10/517,905**

**DATE: 12/22/2004**

**TIME: 16:05:54**

**Input Set : A:\335026.txt**

**Output Set: N:\CRF4\12222004\J517905.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:4793 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
L:4794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:4901 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
L:4972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:10557  
M:341 Repeated in SeqNo=19  
L:10171 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
L:10246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:10328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:10740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:10886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:13371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:2047  
M:341 Repeated in SeqNo=26  
L:13881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:544  
M:341 Repeated in SeqNo=27